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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/062,142DATE: 04/23/98
TIME: 14:53:18

INPUT SET: S25251.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information
4
5 (i) APPLICANT: Sheppard, Paul O.
6
7 (ii) TITLE OF THE INVENTION: SERINE PROTEASE POLYPEPTIDES
8 AND MATERIALS AND METHODS FOR MAKING THEM
9
10 (iii) NUMBER OF SEQUENCES: 16
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: ZymoGenetics, Inc.
14 (B) STREET: 1201 Eastlake Avenue East
15 (C) CITY: Seattle
16 (D) STATE: WA
17 (E) COUNTRY: USA
18 (F) ZIP: 98102
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Diskette
22 (B) COMPUTER: IBM Compatible
23 (C) OPERATING SYSTEM: DOS
24 (D) SOFTWARE: FastSEQ for Windows Version 2.0
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER:
28 (B) FILING DATE:
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER:
33 (B) FILING DATE:
34
35
36
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Parker, Gary E
39 (B) REGISTRATION NUMBER: 31,648
40 (C) REFERENCE/DOCKET NUMBER: 97-16
41
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 206-442-6673
44 (B) TELEFAX: 206-442-6678
45 (C) TELEX:
46

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47
 48 (2) INFORMATION FOR SEQ ID NO:1:
 49
 50 (i) SEQUENCE CHARACTERISTICS:
 51 (A) LENGTH: 1634 base pairs
 52 (B) TYPE: nucleic acid
 53 (C) STRANDEDNESS: double
 54 (D) TOPOLOGY: linear
 55
 56 (ix) FEATURE:
 57
 58 (A) NAME/KEY: Coding Sequence
 59 (B) LOCATION: 105...1280
 60 (D) OTHER INFORMATION:
 61
 62 (A) NAME/KEY: Signal Sequence
 63 (B) LOCATION: 105...161
 64 (D) OTHER INFORMATION:
 65
 66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 67
 68 GGCACGAGGG GGAGCCGCC GCTCTCTCCC GGCGCCCACA CCTGTCTGAG CGGCGCAGCG 60
 69 AGCCGCAGGC CGGGCGGGCT GCTCGGCCGCG GAACAGTGCT CGGC ATG GCA GGG ATT 116
 70 Met Ala Gly Ile
 71
 72 CCA GGG CTC CTC TTC CTT CTC TTC TTT CTG CTC TGT GCT GCT GTT GGG CAA 164
 73 Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys Ala Val Gly Gln
 74 -15 -10 -5 1
 75
 77 GTG AGC CCT TAC AGT GCC CCC TGG AAA CCC ACT TGG CCT GCA TAC CGC 212
 78 Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp Pro Ala Tyr Arg
 79 5 10 15
 80
 81 CTC CCT GTC GTC TTG CCC CAG TCT ACC CTC AAT TTA GCC AAG CCA GAC 260
 82 Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu Ala Lys Pro Asp
 83 20 25 30
 84
 85 TTT GGA GCC GAA GCC AAA TTA GAA GTA TCT TCT TCA TGT GGA CCC CAG 308
 86 Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Cys Gly Pro Gln
 87 35 40 45
 88
 89 TGT CAT AAG GGA ACT CCA CTG CCC ACT TAC AAA GAA GCC AAG CAA TAT 356
 90 Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Lys Glu Ala Lys Gln Tyr
 91 50 55 60 65
 92
 93 CTG TCT TAT GAA ACG CTC TAT GCC AAT GGC AGC CGC ACA GAG ACN CAG 404
 94 Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg Thr Glu Xaa Gln
 95 70 75 80
 96
 97 GTG GGC ATC TAC ATC CTC AGC AGT AGT GGA GAT GGG GCC CAN CNC CGA 452
 98 Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly Ala Xaa Xaa Arg
 99 85 90 95

INPUT SET: S25251.raw

100	GAC TCA GGG TCT TCA GGA AAG TCT CGA AGG AAG CGG CAG ATT TAT GGC	500
101	Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly	
102	100 105 110	
104	TAT GAC AGC AGG TTC AGC ATT TTT GGG AAG GAC TTC CTG CTC AAC TAC	548
105	Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr	
106	115 120 125	
108	CCT TTC TCA ACA TCA GTG AAG TTA TCC ACG GGC TGC ACC GGC ACC CTG	596
109	Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu	
110	130 135 140 145	
112	GTG GCA GAA AAN CAT GTC CTC ACA GCT GCC CAC TGC ATA CAC GAT GGA	644
113	Val Ala Glu Xaa His Val Leu Thr Ala Ala His Cys Ile His Asp Gly	
114	150 155 160	
116	AAA ACC TAT GTG AAA GGA ACC CAG AAG CTT CGA GTC GGC TTC CTA AAG	692
117	Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu Lys	
118	165 170 175	
120	CCC AAG TTT AAA GAT GGT GGT CGA GGG GCC AAC GAC TCC ACT TCA GCC	740
121	Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr Ser Ala	
122	180 185 190	
124	ATG CCC GAG CAG ATG AAA TTT CAG TGG ATC CGG GTG AAA CGC ACC CAT	788
125	Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys Arg Thr His	
126	195 200 205	
128	GTG CCC AAG GGT TGG ATC AAG GGC AAT GCC AAT GAC ATC GGC ATG GAT	836
129	Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp Ile Gly Met Asp	
130	210 215 220 225	
132	TAT GAT TAT GCC CTC CTG GAA CTC AAA AAG CCC CAC AAG AGA AAA TTT	884
133	Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His Lys Arg Lys Phe	
134	230 235 240	
136		
137	ATG AAG ATT GGG GTG AGC CCT CCT GCT AAG CAG CTG CCA GGG GGC AGA	932
138	Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu Pro Gly Gly Arg	
139	245 250 255	
141	ATT CAC TTC TCT GGT TAT GAC AAT GAC CGA CCA GGC AAT TTG GTG TAT	980
142	Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly Asn Leu Val Tyr	
143	260 265 270	
145	CGC TTC TGT GAC GTC AAA GAC GAG ACC TAT GAC TTG TTG TAC CAG CAA	1028
146	Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu Leu Tyr Gln Gln	
147	275 280 285	
149	TGC GAT GCC CAG CCA GGG GCC AGC GGG TAT GGG GTA TAT GTG AGG ATG	1076
150	Cys Asp Ala Gln Pro Gly Ala Ser Gly Tyr Gly Val Tyr Val Arg Met	
151	290 295 300 305	

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/062,142DATE: 04/23/98
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153 TGG AAG AGA CAG CAG AAG TGG GAG CGA AAA ATT ATT GGC ATT TTT 1124
 154 Trp Lys Arg Gln Gln Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe
 155 310 315 320
 157 TCA GGG CAC CAG TGG GTG GAC ATG AAT GGT TCC CCA CAG GAT TTC AAC 1172
 158 Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn
 159 325 330 335
 161 GTG GCT GTC AGA ATC ACT CCT CTC AAA TAT GCC CAG ATC TGC TAT TGG 1220
 162 Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp
 163 340 345 350
 165 ATT AAA GGA AAC TAC CTG GAT TGT AGG GAG GGT GAC ACA GTG TTC CTT 1268
 166 Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp Thr Val Phe Leu
 167 355 360 365
 169 CCT GGC AGC AAT TAAGGTCTTC ATGTTCTTAT TTTAGGAGAG GCCAAATTGT TTTTT 1325
 170 Pro Gly Ser Asn
 171 370
 173 GTCATTGGCG TGCACACGTG TGTGTGTGTG TGTGTGTGTG TGTAAGGTGT CTTATAATCT 1385
 174 TTTACCTATT TCTTACAATT GCAAGATGAC TGGCTTTACT ATTTGAAAAC TGGTTTGTGT 1445
 175 ATCATATCAT ATATCATTAA AGCAGTTGAG AGGCATACTT TTGCATAGAA ATAAAAAAA 1505
 176 TACTGATTTG GGGCAATGAG GAATATTGAG CAATTAAGTT AATCTTCACG TTTTGCAAA 1565
 177 CTTTGATTTT TATTTCATCT GAACTTGTGTT CAAAGATTAA TATTAAATAT TTGGCATAACA 1625
 178 AGAGATATG 1634
 179
 180
 181 (2) INFORMATION FOR SEQ ID NO:2:
 182
 183 (i) SEQUENCE CHARACTERISTICS:
 184 (A) LENGTH: 392 amino acids
 185 (B) TYPE: amino acid
 186 (C) STRANDEDNESS: single
 187 (D) TOPOLOGY: linear
 188
 189 (ii) MOLECULE TYPE: protein
 190 (v) FRAGMENT TYPE: internal
 191 (ix) FEATURE:
 192
 193 (A) NAME/KEY: Signal Sequence
 194 (B) LOCATION: 1...19
 195 (D) OTHER INFORMATION:
 196
 197 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 198
 199 Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys
 200 -15 -10 -5
 201 Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp
 202 1 5 10
 203 Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu
 204 15 20 25
 205 Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser

INPUT SET: S25251.raw

206 30 35 40 45
207 Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Lys Glu
208 50 55 60
209 Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg
210 65 70 75
211 Thr Glu Xaa Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly
212 80 85 90
213 Ala Xaa Xaa Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg
214 95 100 105
215 Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe
216 110 115 120 125
217 Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys
218 130 135 140
219 Thr Gly Thr Leu Val Ala Glu Xaa His Val Leu Thr Ala Ala His Cys
220 145 150 155
221 Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val
222 160 165 170
223 Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp
224 175 180 185
225 Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val
226 190 195 200 205
227 Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
228 210 215 220
229
230 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His
231 225 230 235
232 Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
233 240 245 250
234 Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly
235 255 260 265
236 Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu
237 270 275 280 285
238 Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Tyr Gly Val
239 290 295 300
240 Tyr Val Arg Met Trp Lys Arg Gln Gln Lys Trp Glu Arg Lys Ile
241 305 310 315
242 Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro
243 320 325 330
244 Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln
245 335 340 345
246 Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp
247 350 355 360 365
248 Thr Val Phe Leu Pro Gly Ser Asn
249 370
250
251 (2) INFORMATION FOR SEQ ID NO:3:
252
253 (i) SEQUENCE CHARACTERISTICS:
254 (A) LENGTH: 17 base pairs
255 (B) TYPE: nucleic acid
256 (C) STRANDEDNESS: single
257 (D) TOPOLOGY: linear
258

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/09/062,142**

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Line

Error

Original Text